ATTACHMENT A

Amendments to the Specification

Please amend the marked paragraphs in the manner set forth below:

Please amend the paragraph beginning at Page 9, line 16 as follows:

The LPXTG-motif is identified from the stored sequence information by any of a number of suitable programs. For example, these LPXTG-motif containing proteins can be identified using PHI-blast, which is obtained from NCBI and once again can be installed and stored locally on the SGI or other suitable computer system. The PHI-blast search uses a degenerate LPXTG pattern L-P-X-[TSA]-[GANS] (SEQ ID NO:25), X being any amino acid. The exact templates for PHI-blast can vary depending on the particular organism, but in any case, the present system includes methods of identifying the LPXTG motif. For each organism, it is preferred to use at least two known cell wall anchored proteins of *S. aureus* with no sequence homology as well as known cell wall anchored proteins from the target organism if available.

Please amend the Table beginning at Page 21, line 1 as follows:

TABLE 3. Synthetic oligonucleotides used in this study (SEQ ID NOS:26-43)

Oligonucleotide		Location (aa)	Cloning site	Oligonucleotide
EF1091A	Fw	102	*Sph*I	5'-CC**GCATGC**CAAGAGCAAACAGCAAAAGAAG-3'
	Rev	1107	*Sal*I	5'-CC**GTCGAC***TTA*AGTACCAGAAGTGGTGGTTTTC-3'
EF1824AI	Fw	42	*Sph*I	5'-CC**GCATGC**CAAGAGCAAACAGCAAAAGAAG-3'
	Rev	819	***Sal*I**	5'-GG**GTCGAC***TTA*TTGTTTCAAGGTTACTTCTGTC
EF1824AII	Fw	819	*BamHI*	5'-CC**GGATCC**GCAGCTAATAAAGAAGAATTTTTAG
	Rev	1829	*Sal*I	5'-CC**GTCGAC***TTA*AGTACCAGAAGTGGTGGTTTTC-3'
EF0089A	Fw	35	*Sac*I	5'-CC**GAGCTC**GAAGAGGTTAACAGCGATGG-3'
	Rev	1143	*Pst*I	5'-CC**CTGCAG***TTA*CCCACCAAATGTGATAACCC-3'
EF3023A	Fw	25	*Bam*HI	5'-CC**GGATCC**GAAGAAATAACTGATTTATTTTTAC-3'
	Rev	1024	*Sac*I	5'-CC**GAGCTC***TTA*TTGTTCCTGAATTAATTTTTCTAAC-3'
EF1092A	Fw	27	*Sph*I	5'-CC**GCATGC**TCGCAAGCAAGCGTTCAAG-3'
	Rev	438	*Pst*I	5'-CC**CTGCAG***TTA*GAAGCCTGACTCTTTTACTTTT-3'
EF2224A	Fw	30	*Bam*HI	5'-CC**GGATCC**CAAGAAGTAACAAGTGATGCTG-3'
	Rev	771	*Sac*I	5'-CC**GAGCTC***TTA*AGTTACTTGTTCGTCCGCAAT-3'
EF1269A	Fw	26	*Bam*HI	5'-CC**GGATCC**GAAACAGGATATGCGCAAAC-3'
	Rev	596	*Sac*I	5'-CC**GAGCTC***TTA*TTCCTTATTACGAATCGCCTG-3'
EF1093A	Fw	32	*Bam*HI	5'-GCG**GGATCC**GAAGAAAATGGGGAGAGCGC-3'
	Rev	590	*Sac*I	5'-GCG**GAGCTC***TTA*GGTACCTTTGTGTTTGTTTGG-3'

5' overhang cloning site in each oligonucleotide sequence is marked in bold, stop codon in italic
Fw, oligonucleotide primer in forward direction; Rev, in reverse direction

Please amend the paragraph beginning at Page 60, line 6 as follows:

Primers for flanking regions of sequences above were used to amplify 1µg genomic DNA from each *E. faecalis* strain. PCR products from 5 *E. faecalis* strains in Table 1 were sequenced and compared to the TIGR database sequence. Primers used to amplify the enterococcal MSCRAMM® A-domain gene products are shown below.

Protein	5' Primer	3' Primer
ACE40	GAATTGAGCAAAAGTTCAATCG (SEQ ID NO:44)	GTCTGTCTTTTCACTTGTTTCTGTTG (SEQ ID NO:51)
EF1091	CAAGTAAAAAAGCCGGTACAGC (SEQ ID NO:45)	AAAGGAACCTTTGCTTGGTTC SEQ ID NO:52)
EF1092	TCGCAAGCAAGCGTTCAAG (SEQ ID NO:46)	AAGCCTGACTCTTTTACTTTTTTATTG SEQ ID NO:53)
EF1093	GAGAGCGCACAGCTCGTG (SEQ ID NO:47)	GGTACCTTTGTGTTTGTTTGGTAC SEQ ID NO:54)
Efae2924	CGGGATCCCAAAACAGCGGGAA AGAAATGAGCGA (SEQ ID NO:48)	CCCAAGCTTTCATGTACCTTTGTGTTTA TTTGG (SEQ ID NO:55)
Efae2925	CGGGATCCGAAATGGTTCAGATT ACTTTACAC (SEQ ID NO:49)	TCTGCAGTTCAATTGACTACTTTCAATAT ACTGTC (SEQ ID NO:56)
Efae2926	CGGGATCCAAAGCACTGAACATC AAGCTAAATGCG (SEQ ID NO:50)	CCCAAGCTTTCAGAATGCTTGACCTTGA TTATTGTA (SEQ ID NO:57)